

IN THE CLAIMS:

1. (Currently Amended) A method for identifying the presence of a bacterium in a sample comprising
 - a) testing said sample by Gram-staining and
 - b) testing said sample with a probe according to an *in situ* hybridisation protocolselected on the basis of the outcome of said Gram-staining whether the Gram-staining indicates the presence of a Gram-negative or Gram-positive staining and identifying the presence of the bacterium in the sample.
2. (Original) A method according to claim 1 wherein said sample is a clinical sample.
3. (Previously Amended) A method according to claim 2 wherein said sample is mammalian blood.
4. (Previously Amended) A method according to claim 1 when said Gram-staining indicates the presence of a Gram-negative bacterium in said sample, further comprising determining the rod or coccus character of said bacterium.
5. (Currently Amended) A method according to claim 4 wherein said character is of the rod type, further comprising hybridising said sample with at least one probe selected from a group consisting of probes capable of hybridising with for detecting a nucleic acid found in an organism selected from the group consisting of *Escherichia coli*, *Klebsiella pneumoniae*, *Klebsiella oxytoca*, *Serratia marcescens*, *Enterobacter aerogenes*, *Enterobacter cloacae*, *Proteus vulgaris*, *Proteus mirabilis*, *Salmonella typhi*, and *Pseudomonas aeruginosa*.
6. (Original) A method according to claim 5 wherein said nucleic acid is ribosomal RNA.

7. (Currently Amended) A method according to claim 6 wherein said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence consisting of
GCCTGCCAGTTTCGAATG (SEQ ID NO:1) or;
GTAGCCCTACTCGTAAGG (SEQ ID NO:2) or;
GAGCAAAGGTATTAACCTTACTCCC (SEQ ID NO:3) or; and
GTTAGCCGTCCCTTTCTGG (SEQ ID NO:4).
8. (Original) A method according to claim 4 wherein said character is of the coccus type, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme.
9. (Previously Amended) A method according to claim 1, when said Gram-staining indicates the presence of a Gram-positive bacterium in said sample, further comprising determining the rod or coccus character of said bacterium.
10. (Original) A method according to claim 9 wherein said character is of the rod type, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme and/or Proteinase K.
11. (Previously Amended) A method according to claim 9 wherein said character is of the coccus type, further comprising determining a chain-like or clump-like character of said bacteria.
12. (Original) A method according to claim 11 wherein said character is chain-like, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme.
13. (Currently Amended) A method according to claim 12 further comprising hybridising said sample with at least one probe selected from a group consisting of probes capable of hybridising with for detecting nucleic acid found in an organism selected from the group

14. (Original) A method according to claim 13 wherein said nucleic acid is ribosomal RNA.
15. (Currently Amended) A method according to claim 14 wherein said probe is having no more than five mismatches with a probe selected of a group composed of probes having a sequence TTATCCCCCTCTGATGGG (SEQ ID NO:5) or AGAGAAGCAAGCTTCTCGTCCG (SEQ ID NO:6) or GCCACTCCTCTTTTCCGG (SEQ ID NO:7).
16. (Original) A method according to claim 11 wherein said character is clump-like, further comprising subjecting said sample to treatment with a lysis buffer comprising lysostaphin and/or Proteinase K.
17. (Currently Amended) A method according to claim 16 further comprising hybridising said sample with at least one probe selected from a group consisting of probes capable of hybridising with or detecting nucleic acid found in an organism selected from the group consisting of *Staphylococcus aureus*, *Staphylococcus haemolyticus*, and *Staphylococcus saprophyticus*.
18. (Original) A method according to claim 17 wherein said nucleic acid is ribosomal RNA.
19. (Previously Amended) A method according to claim 18 wherein said probe is having no more than five mismatches with a probe selected of a group consisting of probes having a sequence GCTAATGCAGCGCGGATCC (SEQ ID NO:8) or CCGAAGGGGAAGGCTCTA (SEQ ID NO:9) or AGAGAAGCAAGCTTCTCGTCCGTT (SEQ ID NO:10).
20. (Previously Amended) A method according to claim 4 further comprising hybridising said sample with at least one positive control probe and/or with at least one negative control probe.

21. (Currently Amended) A method according to claim 20 wherein said positive control probe ~~comprising~~comprises no more than five mismatches with a probe with the sequence GCTGCCTCCCGTAGGAGT (SEQ ID NO: 11) and/or wherein said negative control probe comprises no more than five mismatches with a probe with the sequence ACTCCTACGGGAGGCAGC (SEQ ID NO:12).

22. (Currently Amended) A method according to claim 1 further comprising a one-step procedure of binding bacteria present in said sample to a microscopic slide and simultaneously fixing intracellular structures.

23. (Canceled)